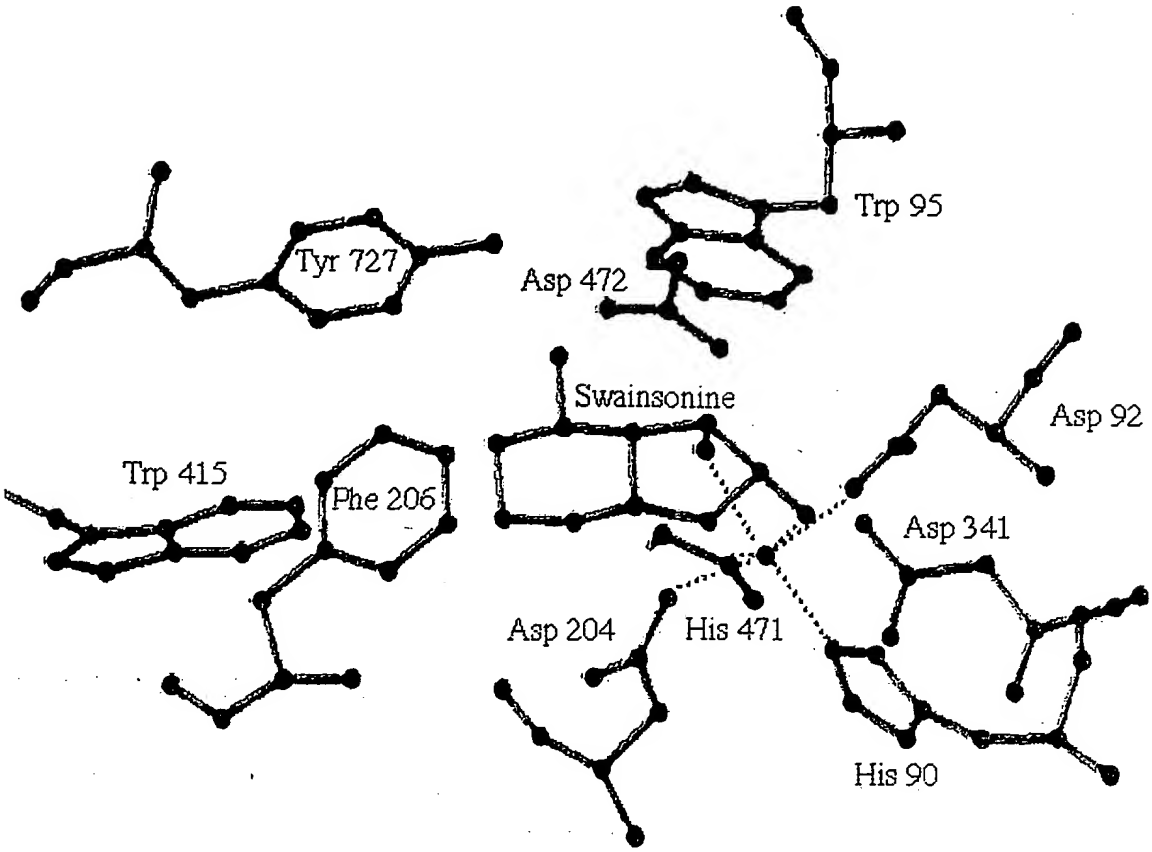
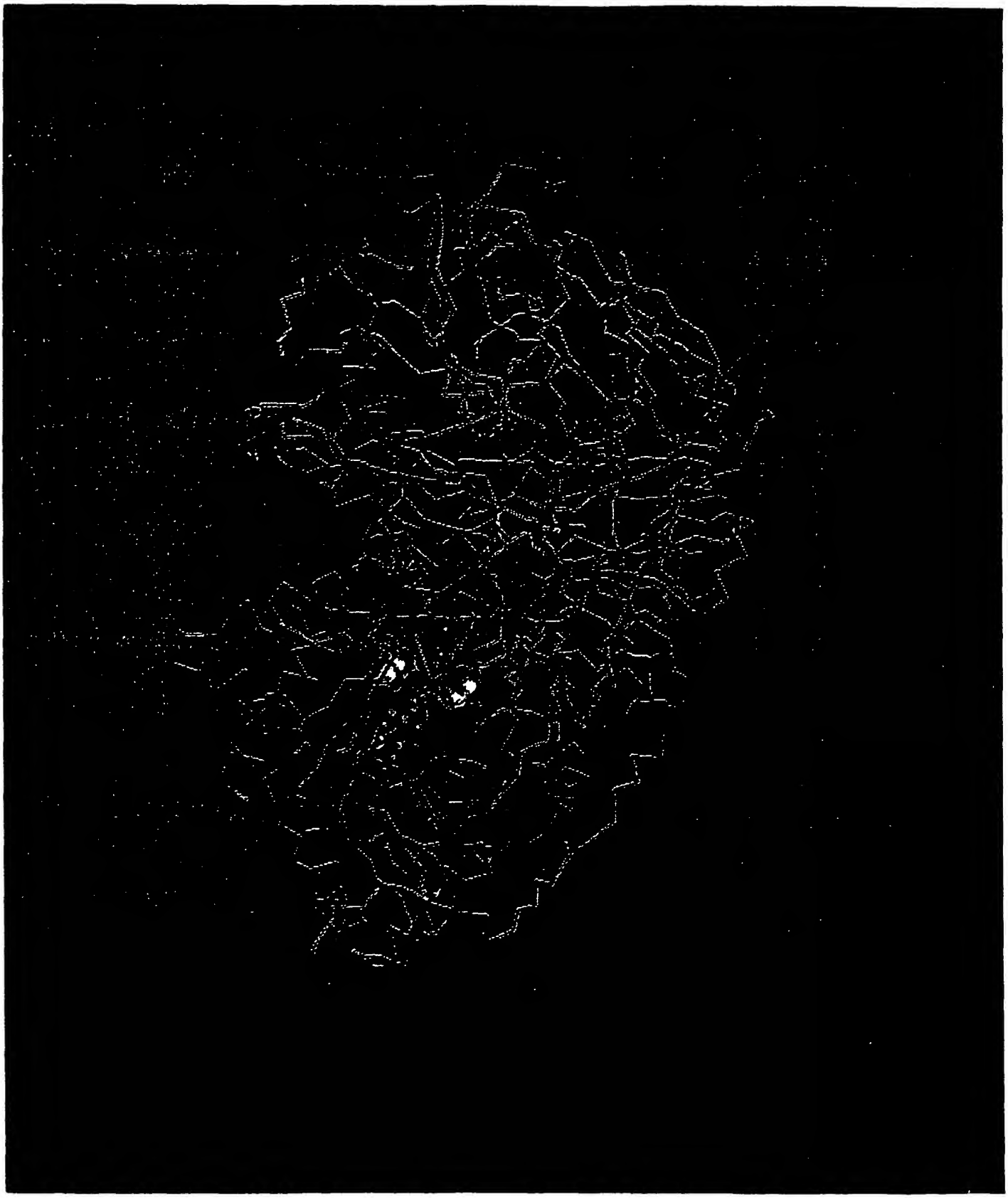
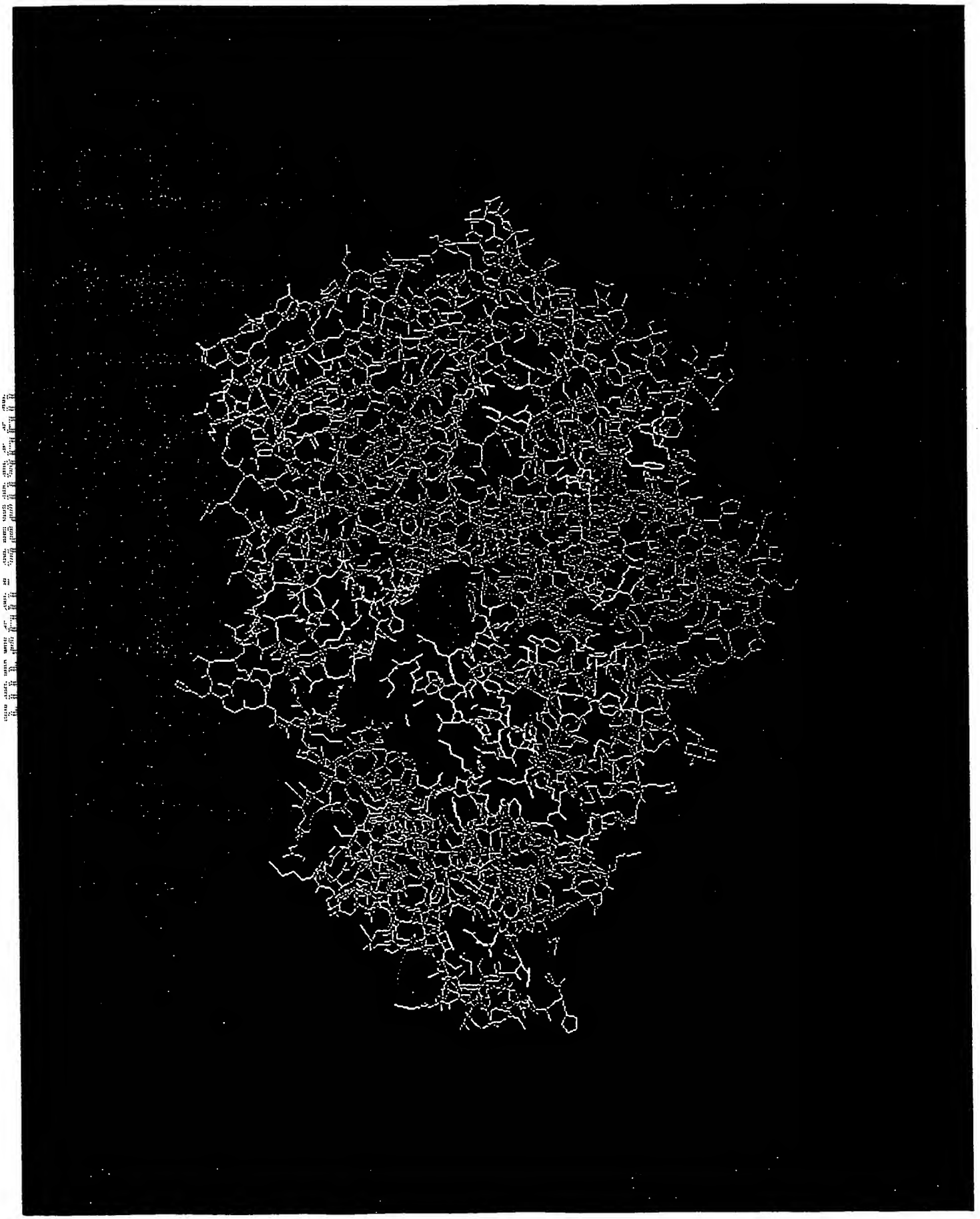
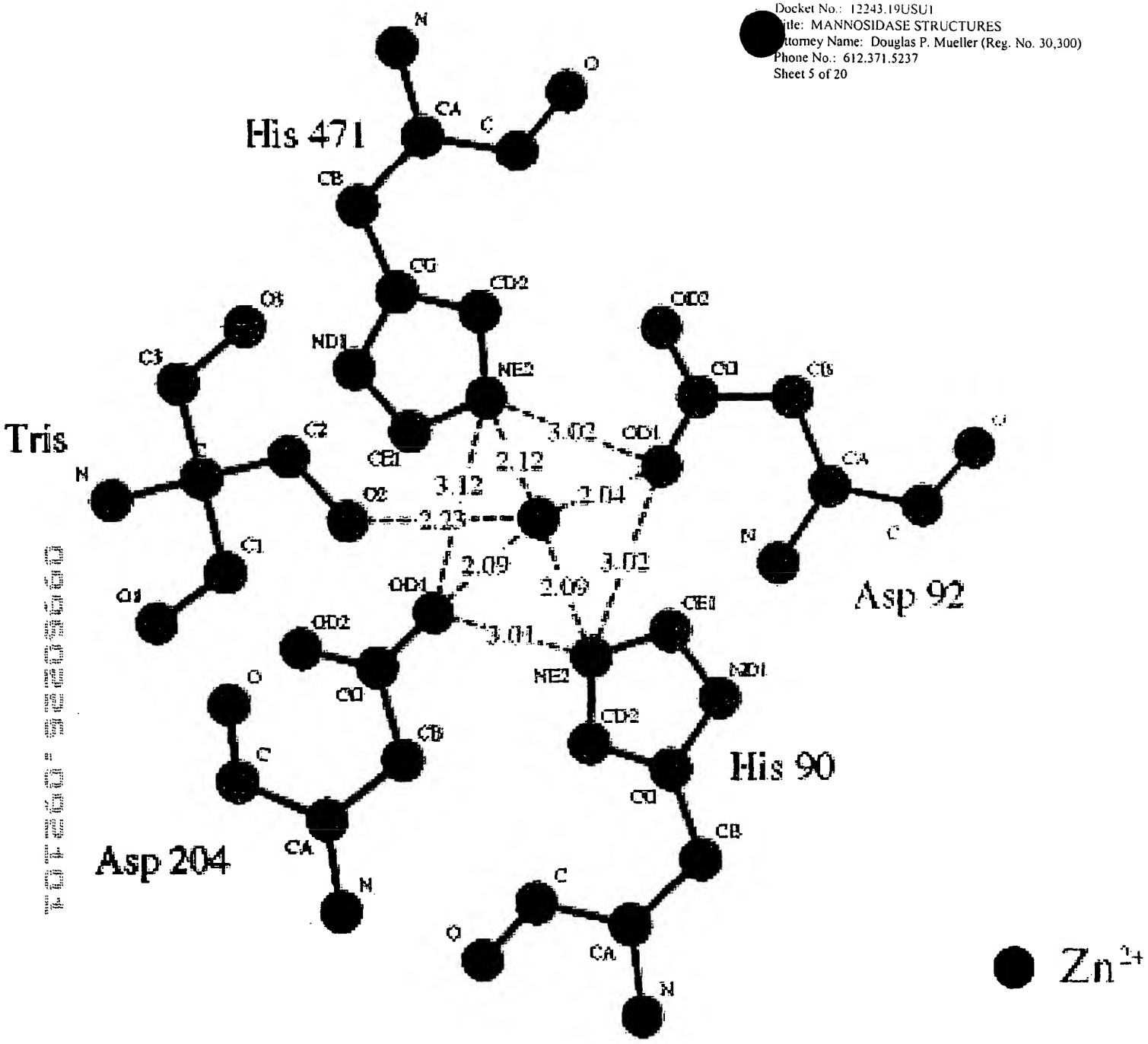

Tyr 727
Trp 95
Asp 472
Swainsonine
Asp 92
Trp 415
Phe 206
Asp 341
Asp 204
His 471
His 90






His 471
Tris
Asp 92
Asp 204
His 90
Zn^{2+}
3.02
2.12
3.12
2.04
2.23
2.09
2.09
3.02
3.01

pMT/BiP-N-HIS-dGMII [851 to 4042] [illegible]-phase Translation

DNA sequence 6642 b.p. TCGCGC[illegible]CG ... AGGCCCTTTCGT circular

N-HIS added to pMTV5HisA (b/t BglII/EcoRI) for drosophilla expression of tagged proteins.
Add drosophila dGMII from clone D11 (shortened 3') DAK/Tara 15-3-99

```
851/1                                   881/11                                  911/21
atg AAG TTA TGC ATA TTA CTG GCC GTC GTG GCC TTT GTT GGC CTC TCG CTC GGG aga tct agc cac cat cat cat cat cac gga gAA TTc
M   K   L   C   I   L   L   A   V   V   A   F   V   G   L   S   L   G   R   S   S   H   H   H   H   H   H   G   E   F
941/31                                  971/41                                  1001/51
gac gat cca ata aga cct cca ctt aaa gtg gct cgt tcc ccg agg cca ggg caa tgc caa gat gtg gtc caa gac gtg ccc aat gtg gat
D   D   P   I   R   P   P   L   K   V   A   R   S   P   R   P   G   Q   C   Q   D   V   V   Q   D   V   P   N   V   D
1031/61                                 1061/71                                 1091/81
gta cag atg ctg gag cta tac gat cgc atg tcc ttc aag gac ata gat gga ggc gtg tgg aaa cag ggc tgg aac att aag tac gat cca
V   Q   M   L   E   L   Y   D   R   M   S   F   K   D   I   D   G   G   V   W   K   Q   G   W   N   I   K   Y   D   P
1121/91                                 1151/101                                1181/111
ctg aag tac aac gcc cat cac aaa cta aaa gtc ttc gtt gtg ccg cac tcg cac aac gat cct gga tgg att cag acg ttt gag gaa tac
L   K   Y   N   A   H   H   K   L   K   V   F   V   V   P   H   S   H   N   D   P   G   W   I   Q   T   F   E   E   Y
1211/121                                1241/131                                1271/141
tac cag cac gac acc aag cac atc ctg tcc aat gca cta cgg cat ctg cac gac aat ccc gag atg aag ttc atc tgg gcg gaa atc tcc
Y   Q   H   D   T   K   H   I   L   S   N   A   L   R   H   L   H   D   N   P   E   M   K   F   I   W   A   E   I   S
1301/151                                1331/161                                1361/171
tac ttt gct cgg ttc tat cac gat ttg gga gag aac aaa aag ctg cag atg aag tcc att gta aag aat gga cag ttg gaa ttt gtg act
Y   F   A   R   F   Y   H   D   L   G   E   N   K   K   L   Q   M   K   S   I   V   K   N   G   Q   L   E   F   V   T
1391/181                                1421/191                                1451/201
gga gga tgg gta atg ccg gac gag gcc aac tcc cac tgg cga aac gta ctg ctg cag ctg acc gaa ggg caa aca tgg ttg aag caa ttc
G   G   W   V   M   P   D   E   A   N   S   H   W   R   N   V   L   L   Q   L   T   E   G   Q   T   W   L   K   Q   F
1481/211                                1511/221                                1541/231
atg aat gtc aca ccc act gct tcc tgg gcc atc gat ccc ttc gga cac agt ccc act atg ccg tac att ttg cag aag agt ggt ttc aag
M   N   V   T   P   T   A   S   W   A   I   D   P   F   G   H   S   P   T   M   P   Y   I   L   Q   K   S   G   F   K
1571/241                                1601/251                                1631/261
aat atg ctt atc caa agg acg cac tat tcg gtt aag aag gaa ctg gcc caa cag cga cag ctt gag ttc ctg tgg cgc cag atc tgg gac
N   M   L   I   Q   R   T   H   Y   S   V   K   K   E   L   A   Q   Q   R   Q   L   E   F   L   W   R   Q   I   W   D
1661/271                                1691/281                                1721/291
aac caa ggg gac aca gct ctc ttc acc cac atg atg ccc ttc tac tcg tac gac att cct cat acc tgt ggt cca gat ccc aag gtt tgc
N   K   G   D   T   A   L   F   T   H   M   M   P   F   Y   S   Y   D   I   P   H   T   C   G   P   D   P   K   V   C
1751/301                                1781/311                                1811/321
tgt cag ttc gat ttc aaa cga atg ggc tcc ttc ggt ttg agt tgt cca tgg aag gtg ccg ccg cgt aca atc agt gat caa aat gtg gca
C   Q   F   D   F   K   R   M   G   S   F   G   L   S   C   P   W   K   V   P   P   R   T   I   S   D   Q   N   V   A
1841/331                                1871/341                                1901/351
gca cgc tca gat ctg ctg gtt gat cag tgg aag aag aag gcc gag ctg tat cgc aca aac gtg ctg ctg att ccg ttg ggt gac gac ttc
A   R   S   D   L   L   V   D   Q   W   K   K   K   A   E   L   Y   R   T   N   V   L   L   I   P   L   G   D   D   F
1931/361                                1961/371                                1991/381
cgc ttc aag cag aac acc gag tgg gat gtg cag cgc gtg aac tac gaa agg ctg ttc gaa cac atc aac agc cag gcc cac ttc aat gtc
R   F   K   Q   N   T   E   W   D   V   Q   R   V   N   Y   E   R   L   F   E   H   I   N   S   Q   A   H   F   N   V
2021/391                                2051/401                                2081/411
cag gcg cag ttc ggc aca ctg cag gaa tac ttt gat gca gtg cac cag gcg gaa agg gcg gga caa gcc gag ttt ccc acg cta agc ggt
Q   A   Q   F   G   T   L   Q   E   Y   F   D   A   V   H   Q   A   E   R   A   G   Q   A   E   F   P   T   L   S   G
2111/421                                2141/431                                2171/441
gac ttt ttc aca tac gcc gat cga tcg gat aac tat tgg agt ggc tac tac aca tcc cgc ccg tat cat aag cgc atg gac cgc gtc ctg
D   F   F   T   Y   A   D   R   S   D   N   Y   W   S   G   Y   Y   T   S   R   P   Y   H   K   R   M   D   R   V   L
2201/451                                2231/461                                2261/471
atg cac tat gta cgt gca gca gaa atg ctt tcc gcc tgg cac tcc tgg gac ggt atg gcc cgc atc gag gaa cgt ctg gag cag gcc cgc
M   H   Y   V   R   A   A   E   M   L   S   A   W   H   S   W   D   G   M   A   R   I   E   E   R   L   E   Q   A   R
2291/481                                2321/491                                2351/501
agg gag ctg tca ttg ttc cag cac cac gac ggt ata act ggc aca gca aaa acg cac gta gtc gtc gac tac gag caa cgc atg cag gaa
R   E   L   S   L   F   Q   H   H   D   G   I   T   G   T   A   K   T   H   V   V   V   D   Y   E   Q   R   M   Q   E
2381/511                                2411/521                                2441/531
gct tta aaa gcc tgt caa atg gta atg caa cag tcg gtc tac cga ttg ctg aca aag ccc tcc atc tac agt ccg gac ttc agt ttc tcg
A   L   K   A   C   Q   M   V   M   Q   Q   S   V   Y   R   L   L   T   K   P   S   I   Y   S   P   D   F   S   F   S
2471/541                                2501/551                                2531/561
tac ttt acg ctc gac gac tcc cgc tgg cca gga tct ggt gtg gag gac agt cga acc acc ata ata ctg ggc gag gat ata ctg ccc tcc
Y   F   T   L   D   D   S   R   W   P   G   S   G   V   E   D   S   R   T   T   I   I   L   G   E   D   I   L   P   S
2561/571                                2591/581                                2621/591
aag cat gtg gtg atg cac aac acc ctg ccc cac tgg cgg gag cag ctg gtg gac ttt tat gta tcc agt ccg ttt gta agc gtt acc gac
K   H   V   V   M   H   N   T   L   P   H   W   R   E   Q   L   V   D   F   Y   V   S   S   P   F   V   S   V   T   D
2651/601                                2681/611                                2711/621
ttg gca aac aat ccg gtg gag gct cag gtg tcc ccg gtg tgg agc tgg cac cac gac aca ctc aca aag act atc cac cca caa ggc tcc
L   A   N   N   P   V   E   A   Q   V   S   P   V   W   S   W   H   H   D   T   L   T   K   T   I   H   P   Q   G   S
2741/631                                2771/641                                2801/651
acc acc aag tac cgc atc atc ttc aag gct cgg gtg ccg ccc atg ggc ttg gcc acc tac gtt tta acc atc tcc gat tcc aag cca gag
T   T   K   Y   R   I   I   F   K   A   R   V   P   P   M   G   L   A   T   Y   V   L   T   I   S   D   S   K   P   E
2831/661                                2861/671                                2891/681
cac acc tcg tat gca tcg aat ctc ttg ctc cgt aaa aac ccg act tcg tta cca ttg ggc caa tat ccg gag gat gtg aag ttt ggc gat
H   T   S   Y   A   S   N   L   L   L   R   K   N   P   T   S   L   P   L   G   Q   Y   P   E   D   V   K   F   G   D
2921/691                                2951/701                                2981/711
cct cga gag atc tca ttg cgg gtt ggt aac gga ccc acc ttg gcc ttt tcg gag cag ggt ctc ctt aag tcc att cag ctt act cag gat
P   R   E   I   S   L   R   V   G   N   G   P   T   L   A   F   S   E   Q   G   L   L   K   S   I   Q   L   T   Q   D
3011/721                                3041/731                                3071/741
agc cca cat gta ccg gtg cac ttc aag ttc ctc aag tat ggc gtt cga tcg cat ggc gat aga tcc ggt gcc tat ctg ttc ctg ccc aat
S   P   H   V   P   V   H   F   K   F   L   K   Y   G   V   R   S   H   G   D   R   S   G   A   Y   L   F   L   P   N
3101/751                                3131/761                                3161/771
gga cca gct tcg cca gtc gag ctt ggc cag cca gtg gtc ctg gtg act aag ggc aaa ctg gag tcg tcc gtg agc gtg gga ctt ccg agc
G   P   A   S   P   V   E   L   G   Q   P   V   V   L   V   T   K   G   K   L   E   S   S   V   S   V   G   L   P   S
3191/781                                3221/791                                3251/801
gtg gtg cac cag acg ata atg cgc ggt ggt gca cct gag att cgc aat ctg gtg gat ata ggc tca ctg gac aac acg gag atc gtg atg
V   V   H   Q   T   I   M   R   G   G   A   P   E   I   R   N   L   V   D   I   G   S   L   D   N   T   E   I   V   M
3281/811                                3311/821                                3341/831
cgc ttg gag acg cat atc gac agc ggc GAT ATC ttc tac acg gat ctc aat gga ttg caa ttt atc aag agg cgg cgt ttg gac aaa tta
R   L   E   T   H   I   D   S   G   D   I   F   Y   T   D   L   N   G   L   Q   F   I   K   R   R   R   L   D   K   L
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3371/841 3401/851 3431/861

cct ttg cag gcc aac tat tat ccc ata cc t ggt atg ttc att gag gat gcc aat acg cga ctc act tc acg ggt caa ccg ctg

P L Q A N Y Y P I P G M F I E D A N T R L T T G Q P L

3461/871 91/881 3521/891

ggt gga tct tct ctg gcc tcg ggc gag cta gag att atg caa gat cgt cgc ctg gcc agc gat gat gaa cgc ggc ctg gga cag ggt gtt

G G S S L A S G E L E I M Q D R R L A S D D E R G L G Q G V

3551/901 3581/911 3611/921

ttg gac aac aag ccg gtg ctg cat att tat cgg ctg gtg ctg gag aag gtt aac aac tgt gtc cga ccg tca aag ctt cat cct gcc ggc

L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G

3641/931 3671/941 3701/951

tat ttg aca agt gcc gca cac aaa gca tcg cag tca ctg ctg gat cca ctg gac aag ttt ata ttc gct gaa aat gag tgg atc ggg gca

Y L T S A A H K A S Q S L L D P L D K F I F A E N E W I G A

3731/961 3761/971 3791/981

cag ggg caa ttt ggt ggc gat cat cct tcg gct cgt gag gat ctc gat gtg tcg gtg atg aga cgc tta acc aag agc tcg gcc aaa acc

Q G Q F G G D H P S A R E D L D V S V M R R L T K S S A K T

3821/991 3851/1001 3881/1011

cag cga gta ggc tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta

Q R V G Y V L H R T N L M Q C G T P E E H T Q K L D V C H L

3911/1021 3941/1031 3971/1041

ctg ccg aat gtg gcg aga tgc gag cgc acg acg ctg act ttc ctg cag aat ttg gag cac ttg gat ggc atg gtg gcg ccg gaa gtg tgc

L P N V A R C E R T T L T F L Q N L E H L D G M V A P E V C

4001/1051 4031/1061

ccc atg gaa acc gcc gct tat gtg agc agt cac tca agc TGA

P M E T A A Y V S S H S S *

Figure 7

ALIGNMENT OF EXPRESSED SECRETED DROSPHILA MANNOSIDASE
WITH HUMAN MANNOSIDASE
Percent Similarity: 52.157 Percent Identity: 43.039

```
   1 .....................................RSSHHHHHHGEFD 13
  51 LQEKIDHLERLLAENNEIISNIRDSVINLSESVEDGPKSSQSNFSQGAGS 100

  14 DPIRPPLKVARSPRPGQCQDVVQD.VPNVDVQMLELYDRMSFKDIDGGVW 62
 101 HLL..PSQLSLSVDTADCLFASQSGSHNSDVQMLDVYSLISFDNPDGGVW 148

  63 KQGWNIKYDPLKYNAHHKLKVFVVPHSHNDPGWIQTFEEYYQHDTKHILS 112
 149 KQGFDITYESNEWDT.EPLQVFVVPHSHNDPGWLKTFNDYFRDKTQYIFN 197

 113 NALRHLHDNPEMKFIWAEISYFARFYHDLGENKKLQMKSIVKNGQLEFVT 162
 198 NMVLKLKEDSRRKFIWSEISYLSKWWDIIDIQKKDAVKSLIENGQLEIVT 247

 163 GGWVMPDEANSHWRNVLLQLTEGQTWLKQFMNVTPTASWAIDPFGHSPTM 212
 248 GGWVMPDEATPHYFALIDQLIEGHQWLENNIGVKPRSGWAIDPFGHSPTM 297

 213 PYILQKSGFKNMLIQRTHYSVKKELAQQRQLEFLWRQIWDNKGDTALFTH 262
 298 AYLLNRAGLSHMLIQRVHYAVKKHFALHKTLEFFWRQNWDLGSVTDILCH 347

 263 MMPFYSYDIPHTCGPDPKVCCQFDFKRMGSFGLSCPWKVPPRTISDQNVA 312
 348 MMPFYSYDIPHTCGPDPKICCQFDFKRLPGGRFGCPWGVPPETIHPGNVQ 397

 313 ARSDLLVDQWKKKAELYRTNVLLIPLGDDFRFKQNTEWDVQRVNYERLFE 362
 398 SRARMLLDQYRKKSKLFRTKVLLAPLGDDFRYCEYTEWDLQFKNYQQLFD 447

 363 HINSQAHFNVQAQFGTLQEYFDAVHQAERA....GQAEFPTLSGDFFTYA 408
 448 YMNSQSKFKVKIQFGTLSDFFDALDKADETQRDKGQSMFPVLSGDFFTYA 497

 409 DRSDNYWSGYYTSRPYHKRMDRVLMHYVRAAEMLSAW.....HSWD.... 449
 498 DRDDHYWSGYFTSRPFYKRMDRIMESHLRAAEILYYFALRQAHKYKINKF 547

 450 GMARIEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRMQEALKACQM 499
 548 LSSSLYTALTEARRNLGLFQHHDAITGTAKDWVVVDYGTRLFHSLMVLEK 597

 500 VMQQSVYRLLTKPSIYSPDFSFSYFTLDDSRWPGSGVEDSRTTIILGEDI 549
 598 IIGNSAFLLIGKDKLTYDSYSPDTFLEMDLKQKSQDSLPQKNIIRLSAE. 646

 550 LPSKHVVMHNTLPHWREQLVDFYVSSPFVSVTDLANNPVEAQVSPVWSWH 599
 647 ..PRYLVVYNPLEQDRISLVSVYVSSPTVQVFSASGKPVEVQVSAVW... 691

 600 HDTLTKTIHPQGSTTKYRIIFKARVPPMGLATYVLTISDSKPEHTSYASN 649
 692 .DT.ANTI....SETAYEISFRAHIPPLGLKVYKILESASS...NSHLAD 732

 650 LLLRKNPTSLPLGQYPEDVKFGDPREISLRVGNGPTLAFSEQGLLKSIQL 699
 733 YVLYKNKVE.DSGIFTIKNMINTEEGITLE.NSFVLLRFDQTGLMKQMMT 780

 700 TQDSPHVPVHFKFLKYGVRSHGDRSGAYLFLPNGPASP.VELGQPVVLVT 748
 781 KEDGKHHEVNVQFSWYGTTIKRDKSGAYLFLPDGNAKPYVYTTPPFVRVT 830
```



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 749 KGKLESSVSVGLPSVVHQTIM......RGGAPEIRNLVDIGSLDNTEIVM 792
 831 HGRIYSEVTCFFDHVTHRVRLYHIQGIEGQSVEVSNIVDIRKVYNREIAM 880

 793 RLETHIDSGDIFYTDLNGLQFIKRRRLDKLPLQANYYPIPSGMFIEDANT 842
 881 KISSDIKSQNRFYTDLNGYQIQPRMTLSKLPLQANVYPMTTMAYIQDAKH 930

 843 RLTLLTGQPLGGSSLASGELEIMQDRRLASDDERGLGQGVLDNKPVLHIY 892
 931 RLTLLSAQSLGVSSLNSGQIEVIMDRRLMQDDNRGLEQGIQDNKITANLF 980

 893 RLVLEKVNNCVRPSKLHPAGYLTSAAHKASQSLLDPL....DKFIFAENE 938
 981 RILLEKRSAVNTEEEKKSVSYPSLLSHITSSLMNHPVIPMANKF...SSP 1027

 939 WIGAQGQFGGDHPSAREDLDVSVMRRLTK..SSAKTQRVGYVLHRTNLMQ 986
1028 TLELQGEFSPLQSSLPCDIHLVNLRTIQSKVGNGHSNEAALILHRKG.FD 1076

 987 C.....GTPE..EHTQ.KLDVCHLLPN..VARCERTTLTFLQNLEHLDGM 1026
1077 CRFSSKGTGLFCSTTQGKILVQKLLNKFIVESLTPSSLSLMHSPPGTQNI 1126

1027 VAPEVCPMETAAYVSSHSS 1045
1127 SEINLSPMEISTFRIQLR. 1144
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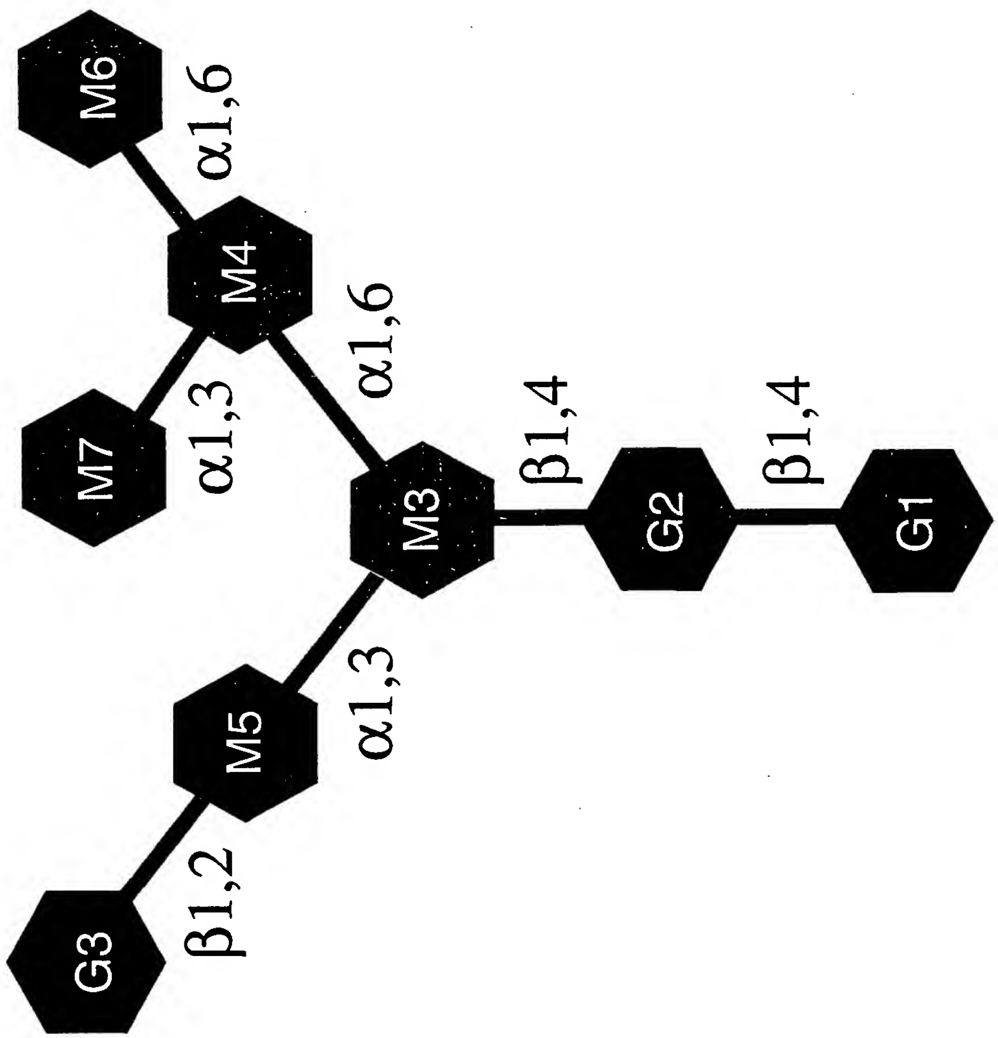
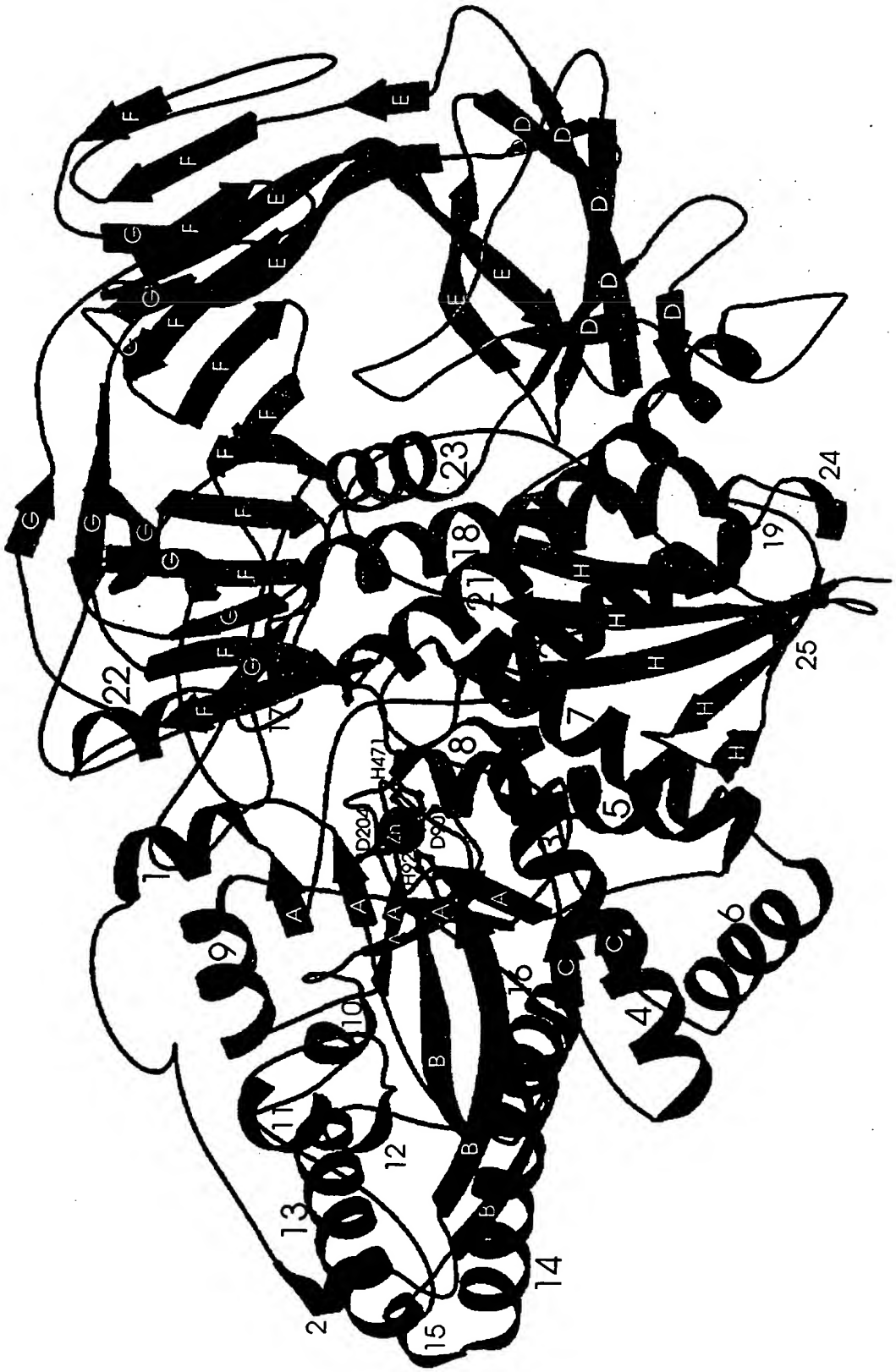


Figure 8A


A
B
C
D
E
F
G
H
1
2
3
4
5
6
7
8
9
10
11
12
13
14
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16
17
18
19
21
22
23
24
25
D204
H471
D92

Figure 8B

Figure 8C

Fig. 9A

Fig. 9B

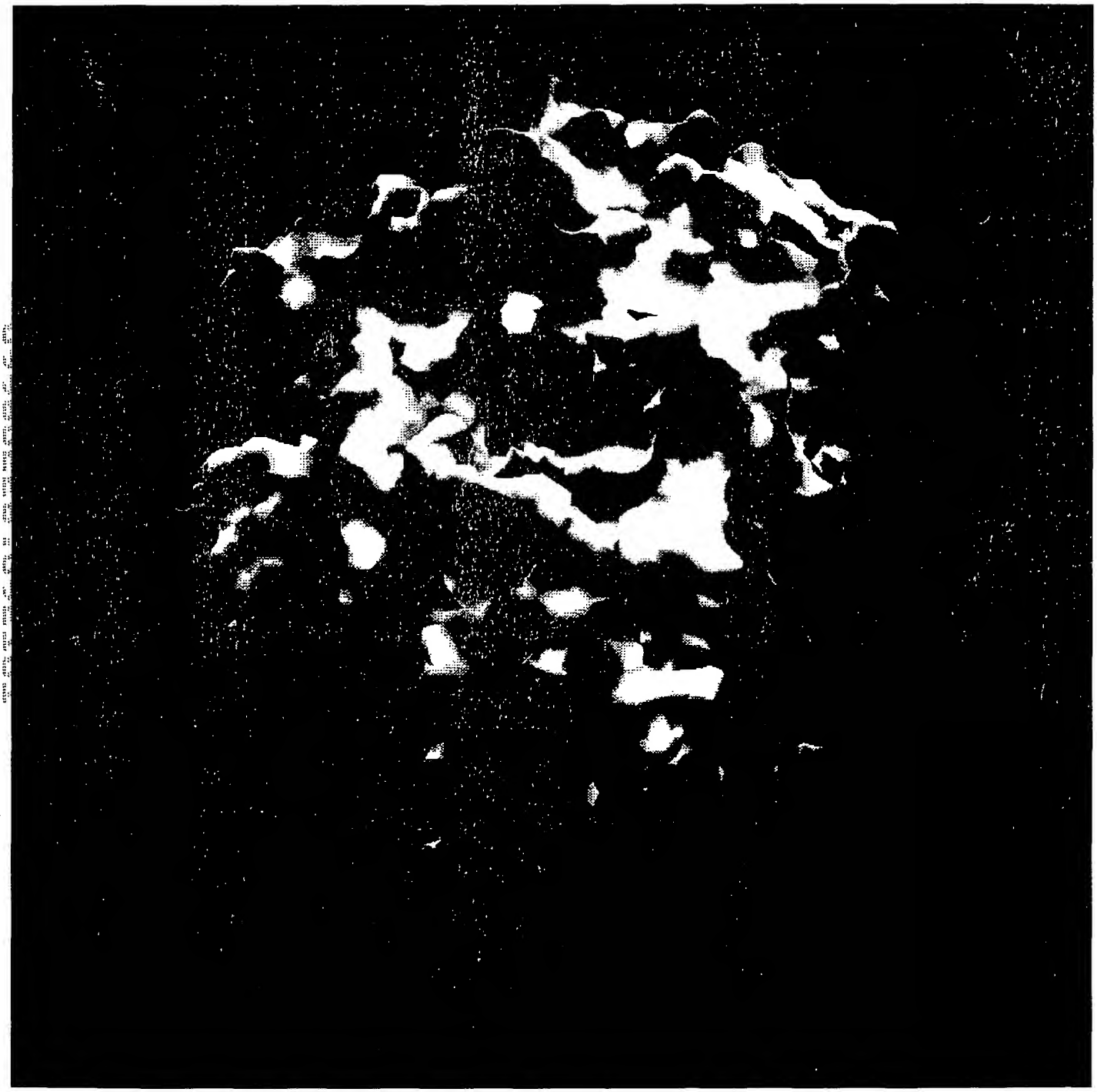
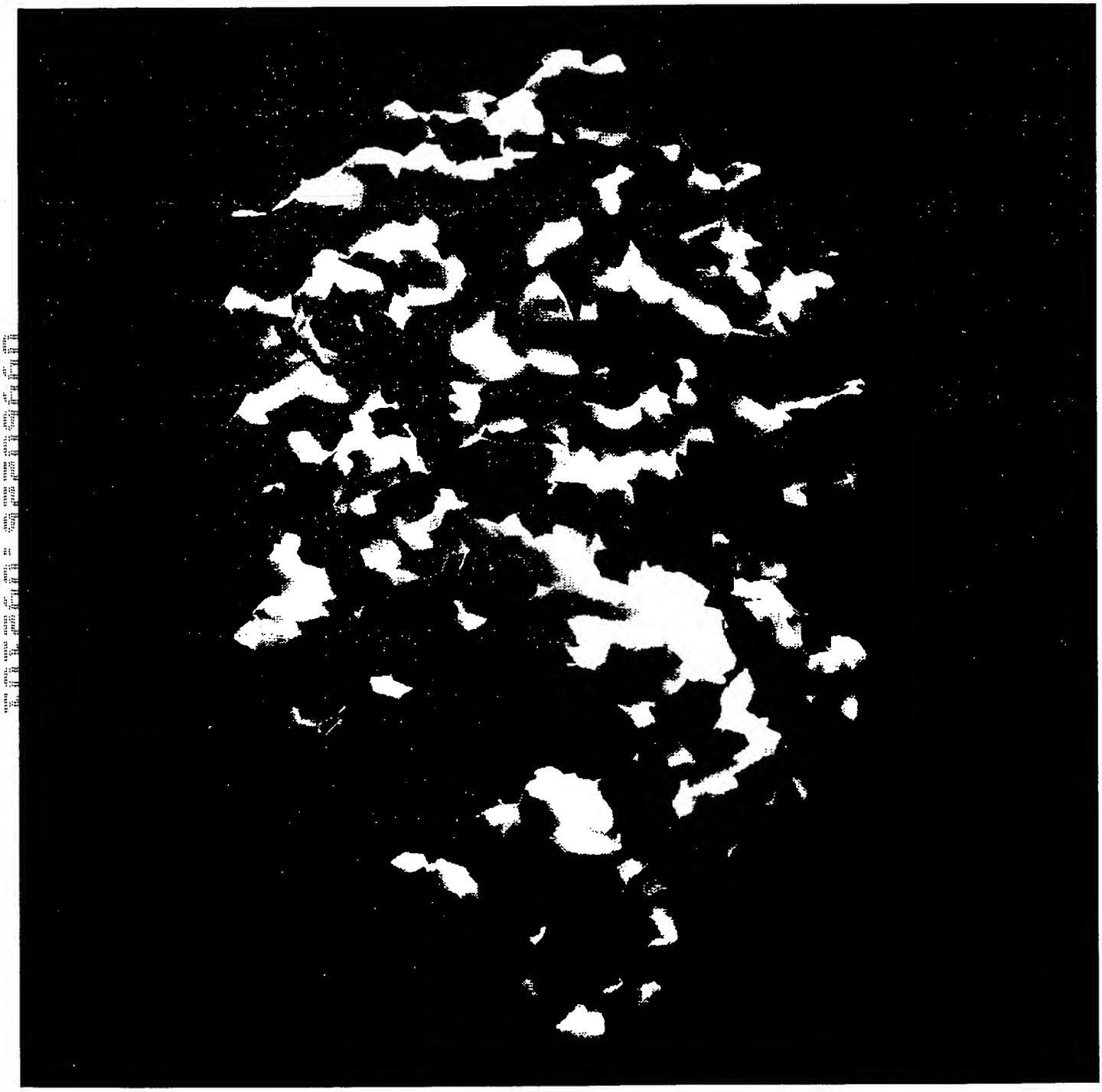
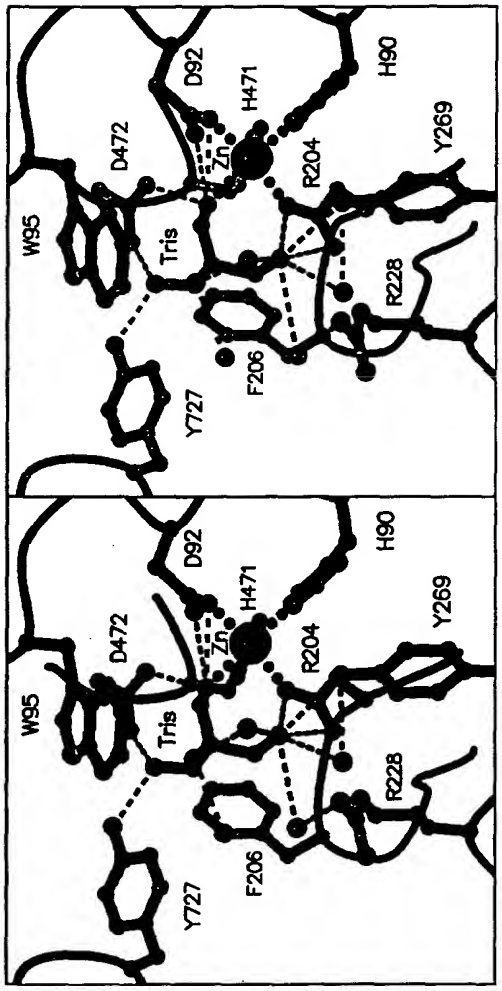


Fig. 9C



Patent Application Publication

Figure 10A



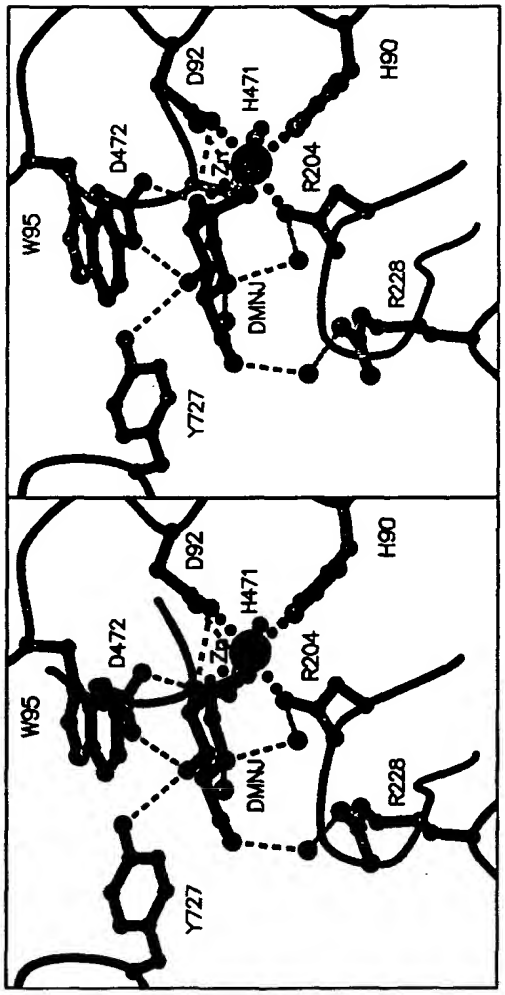


Figure 10B

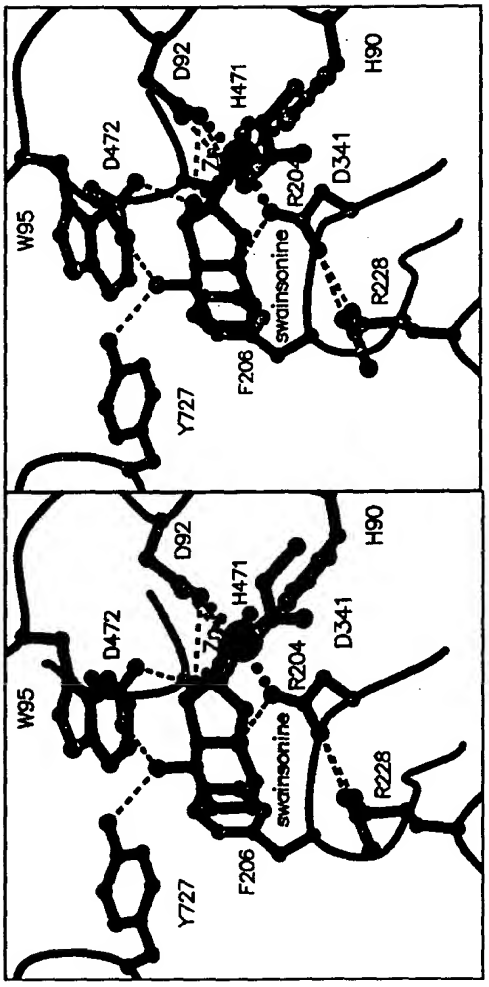
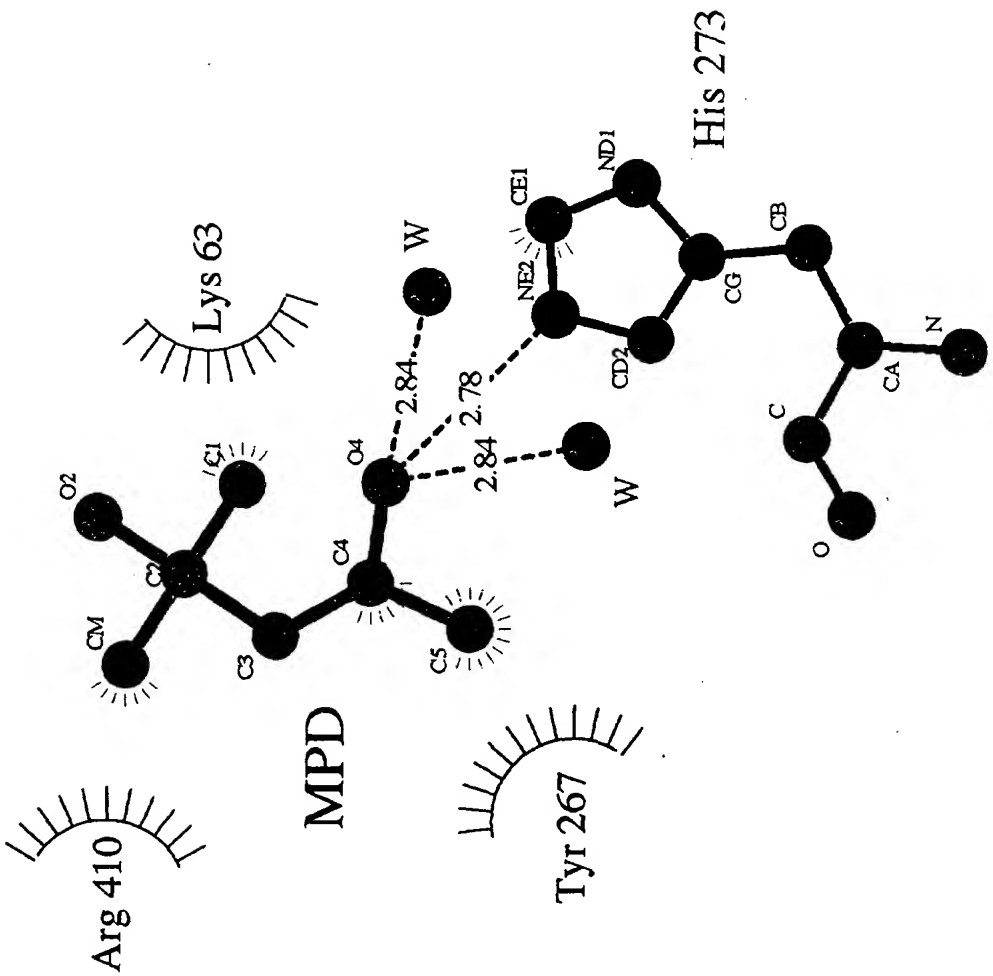


Figure 10C

Figure 11A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2.84
W
His 273
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NE2
CD2
CG
CB
CA
N
C
O
O4
C1
O2
C2
CM
C3
C4
C5
MPD
Arg 410
Tyr 267

Fig. 11B

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Figure 11C